



## SEQUENCE LISTING

<110> Hope, Ralph Graham  
McLauchlan, John

<120> VIRAL THERAPEUTICS

<130> DYOU17.001CP1

<140> US 09/973,322

<141> 2001-10-09

<150> US 09/201,916

<151> 1998-12-01

<150> GB 9825951.8

<151> 1998-11-26

<160> 22

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 630

<212> DNA

<213> Hepatitis C Virus

<220>

<221> CDS

<222> (43)...(630)

<400> 1

ggtgcttgcg agtgccccgg gaggtctcgt agaccgtgca cc atg agc acg aat 54  
Met Ser Thr Asn  
1

cct aaa cct caa aga aaa acc aaa cgt aac acc aac cgt cgc cca cag 102  
Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln  
5 10 15 20

gac gtt aag ttc ccg ggt ggc ggt cag atc gtt ggt gga gtt tac ttg 150  
Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly Gly Val Tyr Leu  
25 30 35

ttg ccg cgc agg ggc cct aga ttg ggt gtg cgc gcg acg agg aag act 198  
Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr  
40 45 50

tcc gag cgg tcg caa cct cga ggt aga cgt cag cct atc ccc aag gca 246  
Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala  
55 60 65

cgt cgg ccc aag ggc agg aac tgg gct cag ccc ggg tat cct tgg ccc 294

Arg	Arg	Pro	Lys	Gly	Arg	Asn	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro		
70						75					80						
ctc	tat	ggc	aat	gag	ggg	tgc	ggg	tgg	gcg	gga	tgg	ctc	ctg	tcc	ccc	342	
Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu	Ser	Pro		
85					90					95					100		
agt	ggc	tct	cgg	cct	agt	tgg	ggc	ccc	aac	gac	ccc	cga	cgt	agg	tcg	390	
Ser	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro	Arg	Arg	Arg	Ser		
				105					110						115		
cgc	aat	ttg	ggg	aag	gtc	atc	gat	acc	ctt	acg	tgc	ggc	ttc	gtc	gat	438	
Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Val	Asp		
			120					125						130			
ctc	atg	ggg	tac	ata	ccg	ctc	gtc	ggc	gcc	cct	ctt	aga	ggc	gct	gcc	486	
Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	Arg	Gly	Ala	Ala		
			135					140						145			
agg	gcc	ctg	gcg	cat	ggc	gtc	cgg	gtt	ctg	gaa	gac	ggg	gtg	aac	tat	534	
Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr		
			150				155				160						
gca	aca	ggg	aac	ctt	cct	ggg	tgc	tct	ttc	tct	atc	ttc	ctt	ctg	gcc	582	
Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala		
165					170					175					180		
ctg	ctc	tct	tgc	ctg	act	gtg	ccc	gct	tca	gcc	tac	caa	gtg	cgc	aac	630	
Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	Tyr	Gln	Val	Arg	Asn		
				185				190							195		

<210> 2  
 <211> 60  
 <212> DNA  
 <213> Hepatitis C Virus

<220>  
 <221> CDS  
 <222> (1)...(60)  
 <223> Corresponds to aa 125 to 144 of SEQ ID. No. 1

<400> 2  
 acc ctt acg tgc ggc ttc gtc gat ctc atg ggg tac ata ccg ctc gtc 48  
 Thr Leu Thr Cys Gly Phe Val Asp Leu Met Gly Tyr Ile Pro Leu Val  
 1 5 10 15

ggc gcc cct ctt 60  
 Gly Ala Pro Leu  
 20

<210> 3  
 <211> 18

<212> DNA  
<213> Hepatitis C Virus

<220>  
<221> CDS  
<222> (1)...(18)  
<223> Corresponds to aa 161-166 of SEQ ID. No. 1

<400> 3  
ggt gtg aac tat gca aca  
Gly Val Asn Tyr Ala Thr  
1 5

18

<210> 4  
<211> 1900  
<212> DNA  
<213> Human

<220>  
<221> misc\_feature  
<222> (1)...(1900)  
<223> n = A,T,C or G

<400> 4  
cgtcttcggg acgcgcccgc tcttcgcctt tcgctgcagt ccgtcgattt ctttctccag 60  
gaagaaaaat ggcattcggt gcagttgac cacaaccgag tgtggtgact cgggtggtca 120  
acctgccctt ggtgagctcc acgtatgacc tcatgtcctc agcctatctc agtacaaagg 180  
accagtatcc ctacctgaag tctgtgtgtg agatgscaga gaacggtgtg aagaccatca 240  
cctccgtggc catgaccagt gctctgcccc tcatccagaa gctagagccg caaattgcag 300  
ttgccgatac ctatgcctgt aaggggctag acaggattga ggagagactg cctattctga 360  
atcagccatc aactcagatt gttgccaatg ccaaaggcgc tgtgactggg gcaaaagatg 420  
ctgtgacgac tactgtgact ggggccaagg attctgtngc cagcacgac acaggggtga 480  
tggacaagac caaaggggca gtgactggca gtgtggagaa gaccaagtct gtggtcagt 540  
gcagcattaa cacagtcttg gggagtcgga tgatgcagct cgtgagcagt ggcgtagaaa 600  
atgcactcac caaatcagag ctgttggtag aacagtacct cctctcact gaggaagaac 660  
tagaaaaaga agcaaaaaaa gttgaaggat ttgatctggt tcagaagcca agttattatg 720  
ttagactggg atccctgtct accaagcttc actcccgctc ctaccagcag gctctcagca 780  
gggttaaaga agctaagcaa aaaagccaac agaccatttc tcagctccat tctactgttc 840  
acctgattga atttgccagg aagaatgtgt atagtgccaa tcagaaaatt caggatgtct 900  
aggataagct ctacctctca tgggtagagt ggaaaaggag cattggatat gatgatactg 960  
atgagtccca ctgtgctgag cacattgagt cacgtactct tgcaattgcc cgcaacctga 1020  
ctcagcagct ccagaccag tgccacaccc tctgttccaa catccaaggt gtaccacaga 1080  
acatccaaga tcaagccaag cacatggggg tgatggcagg cgacatctac tcagtgttcc 1140  
gcaatgctgc ctcttttaa gaagtgtctg acagcctcct cacttctagc aaggggcagc 1200  
tgcagaaaat gaaggaatct ttagatgacg tgatggatta tcttgtaac aacacgcccc 1260  
tcaactggct ggtaggtccc ttttatcttc agctgactga gtctcagaat gctcaggacc 1320  
aaggtgcaga gatggacaag agcagccagg agaccagcg atctgagcat aaaactcatt 1380  
aaacctgccc ctatcactag tgcatgctgt ggccagacag atgacacctt ttgttatgtt 1440  
gaaattaact tgctaggcaa cctaattg ggaagcaagt agctagtata aaggccctca 1500  
attgtagttg tttccagctg aattaagagc tttaaagttt ctggcattag cagatgattt 1560  
ctgttcacct ggtaagaaaa gaatgatagg cttgtcagag cctatagcca gaactcagaa 1620  
aaaattcaaa tgcacttatg ttctcattct atggccattg tggtgcctct gttactgttt 1680  
gtattgaata aaaacatctt catgtgggct ggggtagaaa ctggtgtctg ctctggtgtg 1740  
atctgaaaag gcgtcttcac tgctttatct catgatgctt gcttgtaaaa cttgatttta 1800

gtttttcatt tctcaaatag gaatactacc tttgaattca ataaaaattca ctgcaggata 1860  
gaccagttna gnagcaaaca nncangtaca cnnaaganac 1900

<210> 5  
<211> 437  
<212> PRT  
<213> Human

<220>  
<221> VARIANT  
<222> (1)...(437)  
<223> Xaa = Any Amino Acid

<400> 5  
Met Ala Ser Val Ala Val Asp Pro Gln Pro Ser Val Val Thr Arg Val  
1 5 10 15  
Val Asn Leu Pro Leu Val Ser Ser Thr Tyr Asp Leu Met Ser Ser Ala  
20 25 30  
Tyr Leu Ser Thr Lys Asp Gln Tyr Pro Tyr Leu Lys Ser Val Cys Glu  
35 40 45  
Met Xaa Glu Asn Gly Val Lys Thr Ile Thr Ser Val Ala Met Thr Ser  
50 55 60  
Ala Leu Pro Ile Ile Gln Lys Leu Glu Pro Gln Ile Ala Val Ala Asp  
65 70 75 80  
Thr Tyr Ala Cys Lys Gly Leu Asp Arg Ile Glu Glu Arg Leu Pro Ile  
85 90 95  
Leu Asn Gln Pro Ser Thr Gln Ile Val Ala Asn Ala Lys Gly Ala Val  
100 105 110  
Thr Gly Ala Lys Asp Ala Val Thr Thr Thr Val Thr Gly Ala Lys Asp  
115 120 125  
Ser Val Ala Ser Thr Ile Thr Gly Val Met Asp Lys Thr Lys Gly Ala  
130 135 140  
Val Thr Gly Ser Val Glu Lys Thr Lys Ser Val Val Ser Gly Ser Ile  
145 150 155 160  
Asn Thr Val Leu Gly Ser Arg Met Met Gln Leu Val Ser Ser Gly Val  
165 170 175  
Glu Asn Ala Leu Thr Lys Ser Glu Leu Leu Val Glu Gln Tyr Leu Pro  
180 185 190  
Leu Thr Glu Glu Glu Leu Glu Lys Glu Ala Lys Lys Val Glu Gly Phe  
195 200 205  
Asp Leu Val Gln Lys Pro Ser Tyr Tyr Val Arg Leu Gly Ser Leu Ser  
210 215 220  
Thr Lys Leu His Ser Arg Ala Tyr Gln Gln Ala Leu Ser Arg Val Lys  
225 230 235 240  
Glu Ala Lys Gln Lys Ser Gln Gln Thr Ile Ser Gln Leu His Ser Thr  
245 250 255  
Val His Leu Ile Glu Phe Ala Arg Lys Asn Val Tyr Ser Ala Asn Gln  
260 265 270  
Lys Ile Gln Asp Ala Gln Asp Lys Leu Tyr Leu Ser Trp Val Glu Trp  
275 280 285  
Lys Arg Ser Ile Gly Tyr Asp Asp Thr Asp Glu Ser His Cys Ala Glu  
290 295 300  
His Ile Glu Ser Arg Thr Leu Ala Ile Ala Arg Asn Leu Thr Gln Gln  
305 310 315 320  
Leu Gln Thr Thr Cys His Thr Leu Leu Ser Asn Ile Gln Gly Val Pro



<220>  
 <223> oligonucleotides used to construct HCV core  
 protein deletion plasmids

<400> 8  
 gtaaccttcc tggttgctct tgagatcta 29

<210> 9  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotides used to construct HCV core  
 protein deletion plasmids

<400> 9  
 gtaacctttg agatcta 17

<210> 10  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotides used to construct HCV core  
 protein deletion plasmids

<400> 10  
 ctggcgcatg gagatcta 18

<210> 11  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotides used to construct HCV core  
 protein deletion plasmids

<400> 11  
 ctggcccatg gtgttaacta tgcaacag 28

<210> 12  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotides used to construct HCV core  
 protein deletion plasmids

<400> 12  
 ctggcccatg gcgtccgggt tctggaagac g 31

<210> 13  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> oligonucleotides used to construct HCV core  
           protein deletion plasmids  
  
 <400> 13  
 cgatagaggc gctgccaggg ccctggcgtg agatcta 37  
  
 <210> 14  
 <211> 52  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> HCV1 oligonucleotide for plasmid construction  
  
 <400> 14  
 catgggggtac atagcgctcg tcggcgccgc cttaagaggc gctgcgaggg cc 52  
  
 <210> 15  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> HCV2 oligonucleotide for plasmid construction  
  
 <400> 15  
 ctagagagcg caagacgccc cgcgtcaccg gcggcg 36  
  
 <210> 16  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer derived from GBV-B, nucleotides 428-448,  
           for plasmid construction  
  
 <400> 16  
 ggagatctcg tagaccgtag cacatg 26  
  
 <210> 17  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer derived from GBV-B, nucleotides 842-868,  
           for plasmid construction

<400> 17  
 ggggatccct agtggacacc gaaccaacca gtagccca 38  
  
 <210> 18  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer derived from GBV-B, nucleotides 1003-1029,  
 for plasmid construction  
  
 <400> 18  
 ggggatcctc agatcacaca accaggctcg tgtagg 36  
  
 <210> 19  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer derived from GBV-B, nucleotides 1618-1639,  
 for plasmid construction  
  
 <400> 19  
 ggggtactcta gaggatagg cctggtc 27  
  
 <210> 20  
 <211> 49  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> primer derived from GBV-B for plasmid construction  
  
 <400> 20  
 ctagagagcg caagacgccg cgggtcaccg gtggctctcg caatcttgg 49  
  
 <210> 21  
 <211> 156  
 <212> PRT  
 <213> GBV-B  
  
 <400> 21  
 Met Pro Val Ile Ser Thr Gln Thr Ser Pro Val Pro Ala Pro Arg Thr  
 1 5 10 15  
 Arg Lys Asn Lys Gln Thr Gln Ala Ser Tyr Pro Val Ser Ile Lys Thr  
 20 25 30  
 Ser Val Glu Arg Gly Gln Arg Ala Lys Arg Lys Val Gln Arg Asp Ala  
 35 40 45  
 Arg Pro Arg Asn Tyr Lys Ile Ala Gly Ile His Asp Gly Leu Gln Thr  
 50 55 60  
 Leu Ala Gln Ala Ala Leu Pro Ala His Gly Trp Gly Arg Gln Asp Pro  
 65 70 75 80  
 Arg His Lys Ser Arg Asn Leu Gly Ile Leu Leu Asp Tyr Pro Leu Gly



	85		90		95
Trp Ile Gly Asp Val Thr Thr His Thr Pro Leu Val Gly Pro Leu Val					
100		105		110	
Ala Gly Ala Val Val Arg Pro Val Cys Gln Ile Val Arg Leu Leu Glu					
115		120		125	
Asp Gly Val Asn Trp Ala Thr Gly Trp Phe Gly Val His Leu Phe Val					
130		135		140	
Val Cys Leu Leu Ser Leu Ala Cys Pro Cys Ser Gly					
145	150		155		

<210> 22  
 <211> 191  
 <212> PRT  
 <213> HCV

<400> 22

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn					
1	5	10	15		
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly					
20		25	30		
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala					
35		40	45		
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro					
50	55	60			
Ile Pro Lys Ala Arg Arg Pro Lys Gly Arg Asn Trp Ala Gln Pro Gly					
65	70	75	80		
Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp					
85		90	95		
Leu Leu Ser Pro Ser Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro					
100		105	110		
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys					
115		120	125		
Gly Phe Val Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu					
130		135	140		
Arg Gly Ala Ala Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp					
145	150	155	160		
Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile					
165		170	175		
Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala					
180		185	190		